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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 04:42:12 ; Search time 69 seconds
 (without alignments)
 844.472 Million cell updates/sec

Title: US-09-895-298a-83

Perfect score: 1002

Sequence: 1 MMNFOPPSKANRASQMTFF.....HDSLDRSRRSVQEGNPR 190

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+p2n.model -DEV=x1P
-Q=/cgn2_1/USPIO_spool/US9895298/runat_06112002_160416-2357/app_query.fasta_1.327
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US9895298@CGN_1_1_31@runat_06112002_160416-2357 -NCPU=6 -ICPU=3
-NO_XLPPX -NO_MMW -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database :

```
Issued_Patents_NA.*
```

- 1: /cgn2_5/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	88	8.8 4403765	4	US-09-103-840A-2	Sequence 2, Appli
2	88	8.8 4411529	4	US-09-103-840A-1	Sequence 1, Appli
C 3	86	8.6 1581 2	US-08-845-998-1	Sequence 1, Appli	
C 4	86	8.6 1581 3	US-09-206-537-1	Sequence 1, Appli	
C 5	86	8.6 1581 4	US-09-430-854-1	Sequence 1, Appli	
C 6	85	8.5 1168 4	US-08-858-207A-182	Sequence 182, Appli	
C 7	82.5	8.2 4000 4	US-09-780-049-18	Sequence 18, Appli	
C 8	80	8.0 2555 2	US-08-693-457-3	Sequence 3, Appli	
C 9	80	8.0 2555 4	US-09-265-731-3	Sequence 3, Appli	
10	79.5	7.9 1491 4	US-09-235-451-11	Sequence 11, Appli	
11	79	7.9 1491 4	US-09-134-001C-164	Sequence 164, Appli	
12	78.5	7.8 1812 4	US-09-008-097-3	Sequence 3, Appli	

RESULT 1
 US-09-103-840A-2
 Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; FILE REFERENCE: 2436-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g

Alignment Scores:
 Pred. No.: 3.64e+04
 Score: 88.00
 Percent Similarity: 47.62%

Best Local Similarity: 30.95%
 Query Match: 8.78%
 DB: 4

Gaps: 4

US-09-895-298a-83 (1-190) x US-09-103-840A-2 (1-4403765)

Alignment Scores:
Pred. No.: 5.57
Score: 78.00
Percent Similarity: 34.63%
Best Local Similarity: 20.98%
Query Match: 7.78%

Length: 2243
Matches: 43
Conservative: 28
Mismatches: 56
Indels: 78
Gaps: 9

DB: US-09-895-298A-83 (1-190) x US-07-995-657-1 (1-2243)

QY 19 PhePheIlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrIle---- 36
||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1324 TTTGTCATTTTATCTTCTTCTTCTCTCTGTTTTTG--GTCCTAAGTTATGCCACTG 1380
||||| ::||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 37 -----AlaIleThrIleTrp-----Arg 42
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1381 TAAAGTGAACAGTGTCTGCATGGTCGAAGTAAGCAGTTAGGGCAGCTGTAGT 1440
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 43 LeuLysProSerAlaAspCYSGLyProPheArgGlyLeuProLeuPheIleHisSerIle 62
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1441 ATTAGAAATGCTATTTCCTGTTCCCTTT----- 1470
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 63 TyrSerTripleAspThrLeuSerThrArgProGlyTyroLeuTrp-----ValValTrp 80
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1471 -----CTGCTGGTAGTGATGTCGTG 1491
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrIleLeuValle 100
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 101 IleLeuThrTyrLeuTyrrTrpGlnIleThrGluGlyArgGlyIle----- 115
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1537 -----AAGAAAATUTPAGTTCTAAAAACCG 1560
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 116 -----MetIleArgLeuLeuHisGluGlnIle 124
||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1561 TCGCACCTTCCCTGAGGCTTCCTGTCGCGAGTGACCATGGTGAGGTAGTGTG 1620
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 125 IleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLysLeuGlnAspMet 144
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1621 CTGAACAGCATGCTCTGAAGAGCATGACAATGCTGAGAAAGGGAAACCCCCAACGTCA-TG 1680
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 145 GluLysLysAlaAsnProSerSerIleValleGluArgArgGlyIvaIgIuGlnGlnGly 164
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1681 -----ATTCGGCCATCTCCAAGTCATTATCAAATTCTTCTGATGCAAGAAG 1731
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 165 PheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArgArgSerValGln 184
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1732 CACGGATACATGGAGAGTTCAGTATGTTGATGACCACAGGCCIGGTAAATCGTGGTT 1791
||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 185 GluGlyAsnProArg 189
||| ||||| |||||
Db 1792 GAATTGAACGGTAA 1806
||||| :||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-08-474-587-1
; Sequence 1, Application US/08474587
; Patent No. 5760206
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Perez_Grau, Luis
; TITLE OF INVENTION: Nucleotide Sequence of
; Patent No. 5760206
; TITLE OF INVENTION: Soybean Stearyl-ACP
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; STREET: 1007 Market Street
; CITY: Wilmington

STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19998
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474, 587
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SIEGELL, BARBARA C.
REGISTRATION NUMBER: 30.684
REFERENCE/DOCKET NUMBER: BB_1022-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
LIBRARY: cDNA to mRNA
CLONE: pDS1
FEATURE:
NAME/KEY: 5' non-coding sequence
LOCATION: 1..69
OTHER INFORMATION: /note= "IDENTIFICATION
OTHER INFORMATION: METHOD=Deduced by proximity
OTHER INFORMATION: to location 70-72"
FEATURE:
NAME/KEY: Putative translation initiation codon
LOCATION: 70..72
OTHER INFORMATION: /note= "IDENTIFICATION
METHOD=Similarity of the
OTHER INFORMATION: context of the methionine
OTHER INFORMATION: codon in the open reading frame to translation
FEATURE:
NAME/KEY: Putative transit peptide coding sequence
LOCATION: 70..165
OTHER INFORMATION: /note= "IDENTIFICATION
METHOD=Reduced by proximity
OTHER INFORMATION: to location 70-72 and
OTHER INFORMATION: location 166-1242"
FEATURE:
NAME/KEY: Mature protein coding sequence
LOCATION: 166..1242
OTHER INFORMATION: /note= "IDENTIFICATION
METHOD=Experimental
OTHER INFORMATION: determination of N-terminal
OTHER INFORMATION: amino acid sequence and subunit size of purified soybean
FEATURE:
NAME/KEY: Translation termination codon
LOCATION: 1243..1245
OTHER INFORMATION: /note= "IDENTIFICATION
METHOD=The translation
OTHER INFORMATION: codon ends the open reading
OTHER INFORMATION: frame for a protein of the expected size"

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